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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/625,821	07/22/2003	Satoshi Mori	55022DIV (715.26)	7795
21874 7590 08/05/2009 EDWARDS ANGELL PALMER & DODGE LLP P.O. BOX 55874 BOSTON, MA 02205				
EXAMINER				
KUMAR, VINOD				
ART UNIT		PAPER NUMBER		
1638				
MAIL DATE		DELIVERY MODE		
08/05/2009		PAPER		

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary

Application No.

10/625,821

Applicant(s)

MORI ET AL.

Examiner

VINOD KUMAR

Art Unit

1638

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 08 April 2009.
2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1, 4, 5, 8 and 13-18 is/are pending in the application.
4a) Of the above claim(s) _____ is/are withdrawn from consideration.
5) ☐ Claim(s) _____ is/are allowed.
6) ☒ Claim(s) 1, 4, 5, 8 and 13-18 is/are rejected.
7) ☐ Claim(s) _____ is/are objected to.
8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
10) ☒ The drawing(s) filed on 07 February 2008 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
a) ☒ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☒ Certified copies of the priority documents have been received in Application No. 09/646,825.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08)
Paper No(s)/Mail Date _____
4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date _____
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____

DETAILED ACTION

Status of objections and rejections

1. Applicant's response filed in the paper of 4/8/09 is entered.
2. Claims 1, 4-5, 8, 13-17 and newly added claim 18 are pending. Claims 2-3, 6-7 and 9-12 have been canceled.
3. Newly added claim 18 falls within the scope of currently examined claims. Accordingly, claims 1, 4-5, 8, 13-17 and newly added claim 18 are examined on merits in the present Office action.
4. Objections to claims 1, 8 and 15 have been withdrawn in light of claim amendment filed in the paper of 4/8/09 and upon further consideration by the examiner.
5. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.
6. Rejections of claims 1, 4-5, 8 and 13-17 under 35 U.S.C. 112, 1st paragraph (enablement and written description) have been withdrawn in light of claim amendment and Applicant's persuasive arguments filed in the paper of 4/8/09.
7. Rejections of claims 2 and 9-12 under 35 U.S.C. 112, 1st paragraph (enablement and written description) have been withdrawn in light of cancellation of these claims filed in the paper of 4/8/09.
8. Rejections of claims 9-12 under 35 U.S.C. 103(a) have been withdrawn in light of cancellation of these claims filed in the paper of 4/8/09.

9. Rejection of claims 1, 4-5, 8 and 14-17 under 35 U.S.C. 103(a) as being unpatentable over Perlak et al. (PNAS, 88:3324-3328, April 1991, Applicant's IDS), and further in view of Joshi (Nucleic Acids Research, 15:9627-9640, 1987) is withdrawn in light of amendment to the parent claim 1 filed in the paper of 4/8/09.
10. Rejection of claim 13 under 35 U.S.C. 103(a) as being unpatentable over Perlak et al. (PNAS, 88:3324-3328, April 1991) in view of Joshi (Nucleic Acids Research, 15:9627-9640, 1987), and further in view of D'Halluin et al. (Plant Cell, 4:1495-1505, December 1992) is withdrawn in light of amendment to the parent claim 1 filed in the paper of 4/8/09.

Claim Objections

11. Claims 4, 5 and 17, and newly added claim 18 are objected to because of the following informalities:

Claims 4, 5 and 17 are objected for reciting "GT rich sequence" in line 2. It is suggested to change "GT rich sequence" to --GT rich region-- to maintain consistency with "GT rich region" of the parent claim 1. This objection has been necessitated due to the claim amendment filed in the paper of 4/8/09.

Newly added claim 18 is objected for having improper article before "nucleic acid" in line 1. It is suggested to change "a" to --the--.

Newly added claim 18 is objected for having improper article before "ferric-chelate" in lines 1-2. It is suggested to change "a" to --said--.

Newly added claim 18 is objected for reciting "SEQ ID NO: 1" erroneously. SEQ ID NO: 1 is a nucleotide sequence, whereas SEQ ID NO: 2 is the amino acid sequence. For the purpose of present examination, "SEQ ID NO: 1" recited erroneously would be considered as "SEQ ID NO: 2".

Appropriate action/corrections are requested.

Claim Rejections - 35 USC § 112

12. Claims 4, 5 and 17 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 4, 5 and 17 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite in their recitation "polyadenylation signal sequence" in line 2 because there is insufficient antecedent basis for this limitation in the claims.

This rejection has been necessitated due to the amendments in the parent claim 1 filed in the paper of 4/8/09.

Claim Rejections - 35 USC § 103

13. Claims 1, 4-5, 8 and 14-17 and newly added claim 18 are rejected under 35 U.S.C. 103(a) as being unpatentable over Perlak et al. (PNAS, 88:3324-3328, April 1991) in view of Joshi (Nucleic Acids Research, 15:9627-9640, 1987), and further in view of Dancis et al. (PNAS, 89:3869-3873, Published May 1992) for the reasons of record stated for claims 10-12 (now cancelled) in the Office action mailed 12/8/08. This

rejection has also been necessitated due to the claim amendment filed in the paper of 4/8/09.

Perlak et al. teach a method of making a transgenic plant and seeds derived thereof, comprising introducing and expressing a modified heterologous coding sequence *cryIA(b)* gene of *Bacillus thuringiensis* in transgenic tobacco and tomato plants. The transgenic plants exhibited improved insect resistance. The modification did not alter the amino acid sequence of the heterologous CryIA(b) protein. The modification of coding sequence for *cryIA(b)* comprised altering AATAAA and/or ATTTA sequences. Furthermore, the modification increased G and C content throughout the region of gene to be introduced, and modification was based on plant preferred codons without changing the amino acid sequence. See in particular, page 3324, abstract; page 3324, 2nd paragraph, materials and methods (modification of the coding sequence of insect control genes) through the end of 2nd paragraph of 1st column of page 3325; page 3325, Table 1; page 3326, Figure 1, Table 2; page 3327, Figure 2, Table 3; Page 3328, 1st column, discussion.

Joshi teaches plant gene sequences having GT-rich sequences resembling animal GT-rich sequences found downstream of polyA sites. Joshi also teaches that deletion analysis in the 3' untranslated region of plant mRNA transcripts reveals a region 30 to 80 bases downstream AATAAA comprises GT rich motifs that are also required for correct and efficient polyadenylation of plant mRNA transcripts. See in particular, page 9627, abstract; page 9628, lines 16-31; pgs 9629-9631, table 1.

Perlak et al. or Joshi do not teach FRE1 from yeast.

Dancis et al. teach a nucleic acid sequence which is heterologous to a plant, and encoding yeast ferric-chelate reductase FRE1 (a protein involved in absorption of iron, a plant nutrient). The FRE1 amino acid sequence taught in the reference has 100% identity to instant SEQ ID NO: 2 (incorrectly recited as SEQ ID NO: 1, see claim objection). The nucleic acid sequence taught in the reference comprises internal ATTTA, NATAAA, ANTAAA, AANAAA, AATNAA, AATANA, or AATAAN (wherein N is A, G, C or T) sequences and GT-rich regions which are recognized as polyadenylation signals in plants. See in particular, page 3869, abstract; page 870, figure 1; page 3873 discussion.

It would have been obvious and within the scope of an ordinary skill in the art to modify Perlak et al. method of altering a heterologous nucleic acid sequence by modifying Perlak et al. AATAAA and/or ATTTA sequences and/or Joshi's GT-rich regions present in the coding region of any non-plant heterologous sequence, and which are recognized as plant polyadenylation signal sequences, into some other sequence with a reasonable expectation of success. One of ordinary skill would have been motivated to do so for the purpose of producing a modified heterologous nucleic acid sequence which is devoid of internal polyadenylation signal sequences and encode a full-length and fully functional protein upon expression in a plant.

Given that Joshi teaches that plant GT rich regions are associated with polydenylation process in plants, one of ordinary skill in the art would have been motivated to modify GT rich regions in said heterologous sequence to prevent premature termination of transcription with a reasonable expectation of success.

Given that Joshi clearly asserts the importance of GT rich regions in the polyadenylation of plant mRNA transcripts, it would have been obvious and within the scope of an ordinary skill in the art that any GT rich region including the one having 8 or more consecutive G or T bases would have been scanned and subsequently modified to arrive at the claimed invention with a reasonable expectation of success.

Given that Dancis et al. teach a heterologous sequence from yeast encoding FRE1 which is involved in the absorption of nutrients, it would have been obvious and within the scope of an ordinary skill in the art to modify internal AATAAA and/or ATTTA sequences, and/or GT-rich regions of Dancis et al. FRE1 coding sequence to some other sequences that are not recognized as plant polyadenylation signal sequences, using the teachings of Perlak et al. and Joshi as discussed above. One of ordinary skill in the art would have been motivated to do so for the purpose of over-expressing a full-length yeast FRE1 protein in transgenic plants to increase absorption of iron (a nutrient) in said plants with a reasonable expectation of success.

14. Applicant's arguments & response from the examiner:

In the paper filed 4/8/09, Applicant argues that Dancis et al. do not teach GT rich region of FRE1 coding sequence. Applicant further argues that GT rich regions of Dancis et al. FRE1 are present in the promoter sequence, wherein GT regions of the presently claimed invention is in coding region of FRE1 (response, page 8, lines 1-9).

Applicant's arguments have been carefully considered but are deemed to be unpersuasive.

Applicant's attention is drawn to figure 1 (page 3870) of Dancis et al., wherein the reference clearly teaches the complete coding sequence and the encoded FRE1 protein having 100% identity to instant SEQ ID NO: 2 (incorrectly recited as SEQ ID NO: 1, see claim objection). The nucleic acid sequence taught in the reference is heterologous to a plant because it encodes yeast ferric-chelate reductase FRE1 (a protein involved in absorption of iron, a plant nutrient). The nucleic acid sequence taught in the reference comprises internal ATTTA, NATAAA, ANTAAA, AANAAA, AATNAA, AATANA, or AATAAN (wherein N is A, G, C or T) sequences and GT rich regions (see figure 1) which are recognized as polyadenylation signals in plants. See in particular, page 3869, abstract; page 870, figure 1; page 3873 discussion.

Applicant further argues that Perlak et al. do not teach that GT rich sequence could be a polyadenylation signal in a combination of ATs. Applicant further argues that Perlak et al. disclose modification of prokaryotic organism gene cryIA(b) and introduction into a plant. Applicant further argues that ATTTA sequence or potential polyadenylation signal sequence (AATAAA or AATAAT) that were present in coding sequence of cryIA(b) gene were modified, thereby resulting to increase G+C content and plant preferred codons, and not to generate 6 or more A+T or G+C. Applicant also argues that Perlak et al. do not teach how to modify the yeast FRE1 gene or how to modify 8 or more consecutive nucleotide consisting of G or T (response, page 8, lines 10-24).

Applicant's arguments have been carefully considered but are deemed to be unpersuasive.

Applicant's attention is drawn to page 3324, abstract; page 3324, 2nd paragraph, materials and methods (modification of the coding sequence of insect control genes) through the end of 2nd paragraph of 1st column of page 3325; page 3325, table 1; page 3326, figure 1, table 2; page 3327, figure 2, table 3; page 3328, 1st column, discussion; wherein Perlak et al. clearly teach a method of making a transgenic plant and seeds derived thereof, comprising introducing and expressing a modified coding sequence *cryIA(b)* gene of *Bacillus thuringiensis* in transgenic tobacco and tomato plants. The transgenic plants exhibited improved insect resistance. The modification did not alter the amino acid sequence of the CryIA(b) protein. The modification of coding sequence for *cryIA(b)* comprised altering AATAAA and/or ATTTA sequences. Furthermore, the modification increased G and C content throughout the region of gene to be introduced, and modification was based on plant preferred codons without changing the amino acid sequence.

It is important to note that the issue is not whether Perlak et al. should teach FRE1 from yeast because that deficiency is overcome by the teachings of Dancis et al. as discussed above (see rejection). Also, the issue is not whether G+C content is increased because instantly claimed method does not require whether the modified heterologous nucleic acid sequence has increased G+C content compared to an unmodified heterologous nucleic acid sequence.

Rather, the issue is whether one of ordinary skill in the art would have known that sequences ATTTA, NATAAA, ANTAAA, AANAAA, AATNAA, AATANA, or AATAAN (wherein N is A, G, C or T) and GT rich regions present in a heterologous coding

sequence would be recognized as potential polyadenylation signal sequences in plants. Perlak et al. teachings clearly would have suggested to one of ordinary skilled in the art at the time the instantly claimed invention was made, that heterologous coding sequences (e.g. cryIA(b)) obtained from organisms other than plant comprise internal sequences such as, AATAAA or ATTTA which are recognized as polyadenylation signal sequences upon expression in a plant environment. Likewise, Joshi's teachings would have suggested to one of ordinary skill in the art that GT regions present in a heterologous nucleic acid sequence are recognized as polyadenylation signal sequences upon expression in a plant environment. Furthermore, Perlak et al. teachings would have also provided the necessary method steps to modify said internal polydenylation signals so that the modified hetrologous nucleic acid sequence encodes the full-length protein upon expression in a plant system. For these reasons, Applicant's arguments are not on point.

Applicant further argues that Joshi provides no teachings related to iron assimilation and further alleges that Joshi only teaches 5 consecutive G and/or T residues, not 8 as required in the instant claims. Applicant while admitting that Joshi teaches AATAAA, continues to argue that the reference fails to teach the importance of GT rich regions in polyadenylation of higher plants (response, page 9, lines 7-21).

It is important to note that the issue is not whether Joshi et al. should teach FRE1 from yeast because that deficiency is overcome by the teachings of Dancis et al. as discussed above in the rejection.

Applicant attention is drawn to page 9627, abstract; page 9628, lines 16-31; pages 9629-9631, table 1, wherein Joshi clearly teaches plant gene sequences having GT-rich sequences resembling heterologous (e.g. animal) GT-rich sequences found downstream of polyA sites. Joshi also teaches that deletion analysis in the 3' untranslated region of plant mRNA transcripts reveals a region 30 to 80 bases downstream AATAAA comprises GT rich motifs that are also required for correct and efficient polyadenylation of plant mRNA transcripts. This clearly implies that Joshi does teach that GT rich motifs (or regions) are recognized as polydenylation signals in plants.

It would have been obvious and within the scope of an ordinary skill in the art to modify the method of altering heterologous nucleic acid sequence as taught by Perlak et al. by modifying internal plant polyadenylation signals that comprises AATAAA and/or ATTTA and GT rich regions as taught by Joshi to some other sequence that are not recognized as plant polyadenylation signals.

Given that Joshi teaches that plant GT rich regions are associated with polydenylation process in plants, one of ordinary skill in the art would have been motivated to modify GT rich regions in said heterologous sequence to prevent premature termination of transcription with a reasonable expectation of success.

Given that Joshi clearly asserts the importance of GT rich regions in the polyadenylation of plant mRNA transcripts, it would have been obvious that any GT rich region including the one having 8 or more consecutive G or T nucleotides would have been scanned and subsequently modified by an ordinary skill in the art to arrive at the claimed invention with a reasonable expectation of success.

Given that Dancis et al. teach (i) a heterologous sequence from yeast encoding FRE1 which is involved in the absorption of iron (a plant nutrient), and (ii) yeast FRE1 coding sequence which contains internal sequences, such as, ATTTA, NATAAA, ANTAAA, AANAAA, AATNAA, AATANA, or AATAAN (wherein N is A, G, C or T), and GT rich regions, and which are recognized as potential polyadenylation signals in plants as asserted by Perlak et al. and Joshi, it would have been obvious and within the scope of an ordinary skill in the art to modify said internal sequences present within Dancis et al. FRE1 coding sequence to some other sequence to prevent premature termination of transcription upon expression in a plant. One of ordinary skill in the art would have been motivated to do so for the purpose of over-expressing the full-length yeast FRE1 protein in a plant to increase absorption of iron (a nutrient) by said plant with a reasonable expectation of success.

Applicant also alleges that there can be no motivation to combine the references other than by use of impermissible hindsight. Applicant further alleges that there is not teaching or suggestions in any of the references to modify yeast FRE1 for expression in plants based on the cited references (response, page 10, lines 5-23).

Applicant's arguments are fully carefully considered but are deemed to be unpersuasive.

In response to applicant's argument that there is no suggestion to combine the references, the examiner recognizes that obviousness can only be established by combining or modifying the teachings of the prior art to produce the claimed invention where there is some teaching, suggestion, or motivation to do so found either in the

references themselves or in the knowledge generally available to one of ordinary skill in the art. See *In re Fine*, 837 F.2d 1071, 5 USPQ2d 1596 (Fed. Cir. 1988) and *In re Jones*, 958 F.2d 347, 21 USPQ2d 1941 (Fed. Cir. 1992). In this case, given that Dancis et al. teach a heterologous sequence from yeast encoding FRE1 which is involved in the absorption of nutrients, and given Dancis et al. FRE1 sequence contains internal sequences, such as, ATTTA, NATAAA, ANTAAA, AANAAA, AATNAA, AATANA, or AATAAN (wherein N is A, G, C or T), and GT rich regions, it would have been obvious and within the scope of an ordinary skill in the art to modify internal AATAAA and/or ATTTA sequences and/or GT-rich regions of Dancis et al. FRE1 coding sequence to some other sequences that are not recognized as polyadenylation signals in plants, using the teachings of Perlak et al. and Joshi as discussed above. One of ordinary skill in the art would have been motivated to do so for the purpose of over-expressing full-length FRE1 protein to increase absorption of iron (a nutrient) in transgenic plants with a reasonable expectation of success. Thus, one of ordinary skill in the art would have arrived at the claimed invention with a reasonable expectation of success by combining the teachings of Perlak et al., Joshi and Dancis et al. as discussed above.

In response to Applicant's argument that Joshi does not teach 8 or more consecutive G and/or T nucleotides, Applicant is reminded that the test for obviousness is not whether the features of a secondary reference may be bodily incorporated into the structure of the primary reference; nor is it that the claimed invention must be expressly suggested in any one or all of the references. Rather, the test is what the combined teachings of the references would have suggested to those of ordinary skill in the art.

See *In re Keller*, 642 F.2d 413, 208 USPQ 871 (CCPA 1981). In the instant case, given Perlak et al. and Joshi et al. teachings when combined together would have suggested to an ordinary skill in the art that GT-rich regions in combination with AATAAA and/or ATTTA sequences were implicated in polyadenylation at the time the invention was claimed, it would have been obvious to modify heterologous coding sequences having internal AATAAA and/or ATTTA sequences and GT-rich regions to prevent premature termination of the transcript when expressed in a plant with a reasonable expectation of success.

It is important to note that Obviousness does not require an absolute certainty of success but merely a reasonable expectation thereof, so long as the motivation or suggestion to combine the teaching of the cited references is known or disclosed in the prior art and is obvious to one skilled in the art and this is sufficient to establish a *prima facie* case of obviousness.

Thus, it is maintained that the claimed invention as a whole is *prima facie* obvious over the combined teachings of the prior art.

15. Claim 13 is rejected under 35 U.S.C. 103(a) as being unpatentable over Perlak et al. (PNAS, 88:3324-3328, April 1991) in view of Joshi (Nucleic Acids Research, 15:9627-9640, 1987), and Dancis et al. (PNAS, 89:3869-3873, Published May 1992) as applied to claims 1, 4-5, 8 and 14-17 above, and further in view of D'Halluin et al. (Plant Cell, 4:1495-1505, December 1992) for the reasons of record stated in the Office action mailed 12/8/08. This rejection has also been necessitated due to the claim amendment filed in the paper of 4/8/09.

Perlak et al. teachings are discussed *supra*.

Joshi's teachings are discussed *supra*.

Dancis et al. teachings are discussed *supra*.

Perlak et al., Joshi or Dancis et al. do not teach transforming a gramineae (monocotyledonous) plant.

D'Halluin et al. teach a method of transforming a maize plant. Maize is a monocotyledonous plant belonging to family gramineae. See in particular, pg 1495, abstract; pgs 1503-1504, materials and methods.

It would have been obvious and within the scope of an ordinary skill in the art to over-express a modified heterologous DNA (modified by changing internal AATAAA and/or ATTTA sequences and GT rich regions to some other sequence that are not recognized as polyadenylation signals in plants as taught by Perlak et al. and Joshi) encoding any economically important protein including yeast FRE1 protein of Dancis et al., in any plant species including an economically important maize plant using any method of plant transformation, including the plant transformation method of D'Halluin et al. One of ordinary skill in the art would have been motivated to do so for the purpose of increasing iron (important plant nutrient) absorption in said plant of gramineae family with a reasonable expectation of success.

It is noted that Applicant did not file separate arguments for the 103(a) rejection for claim 13 made in the Office action mailed 12/8/2008.

Conclusions

16. Claims 1, 4-5, 8 and 13-18 are rejected.

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Contact Information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to VINOD KUMAR whose telephone number is (571)272-4445. The examiner can normally be reached on 8.30 a.m. to 5.00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg can be reached on (571) 272-0975. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Vinod Kumar/
Examiner, Art Unit 1638